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DATE: 02/06/2002
TIME: 08:50:53RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/654,281BInput Set : A:\ES.txt
Output Set: N:\CRF3\02062002\I654281B.raw

3 <110> APPLICANT: Sedivy, John
 4 ' Kolch, Walter
 5 Yeung, Kam Chi
 7 <120> TITLE OF INVENTION: Kinase Inhibitors and Methods of Use in Screening Assays and Modulation
 8 of Cell Proliferation and Growth
 10 <130> FILE REFERENCE: 3564/1010
 12 <140> CURRENT APPLICATION NUMBER: 09/654,281B
 13 <141> CURRENT FILING DATE: 2000-09-01
 15 <150> PRIOR APPLICATION NUMBER: 60/151,992
 16 <151> PRIOR FILING DATE: 1999-09-01
 18 <160> NUMBER OF SEQ ID NOS: 11
 20 <170> SOFTWARE: PatentIn version 3.1
 22 <210> SEQ ID NO: 1
 23 <211> LENGTH: 94
 24 <212> TYPE: PRT
 25 <213> ORGANISM: Artificial Sequence
 27 <220> FEATURE:
 28 <223> OTHER INFORMATION: consensus sequence
 30 <220> FEATURE:
 31 <221> NAME/KEY: MISC_FEATURE
 32 <222> LOCATION: (3)..(5)
 33 <223> OTHER INFORMATION: Xaa = any amino acid
 36 <220> FEATURE:
 37 <221> NAME/KEY: MISC_FEATURE
 38 <222> LOCATION: (9)..(9)
 39 <223> OTHER INFORMATION: a hydrophobic amino acid residue
 42 <220> FEATURE:
 43 <221> NAME/KEY: MISC_FEATURE
 44 <222> LOCATION: (11)..(13)
 45 <223> OTHER INFORMATION: Xaa = any amino acid
 48 <220> FEATURE:
 49 <221> NAME/KEY: MISC_FEATURE
 50 <222> LOCATION: (14)..(14)
 51 <223> OTHER INFORMATION: a negatively charged amino acid residue
 54 <220> FEATURE:
 55 <221> NAME/KEY: MISC_FEATURE
 56 <222> LOCATION: (15)..(18)
 57 <223> OTHER INFORMATION: Xaa = any amino acid residue
 60 <220> FEATURE:
 61 <221> NAME/KEY: MISC_FEATURE
 62 <222> LOCATION: (20)..(21)
 63 <223> OTHER INFORMATION: Xaa = any amino acid residue
 66 <220> FEATURE:

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67 <221> NAME/KEY: MISC_FEATURE
 68 <222> LOCATION: (23)..(72)
 69 <223> OTHER INFORMATION: Xaa = any amino acid residue, 0 to 40 residues may be missing
 72 <220> FEATURE:
 73 <221> NAME/KEY: MISC_FEATURE
 74 <222> LOCATION: (74)..(77)
 75 <223> OTHER INFORMATION: Xaa = any amino acid residue
 78 <220> FEATURE:
 79 <221> NAME/KEY: MISC_FEATURE
 80 <222> LOCATION: (79)..(82)
 81 <223> OTHER INFORMATION: Xaa = any amino acid residue, 0 to 2 residues may be missing
 84 <220> FEATURE:
 85 <221> NAME/KEY: MISC_FEATURE
 86 <222> LOCATION: (84)..(84)
 87 <223> OTHER INFORMATION: Xaa = any amino acid residue
 90 <220> FEATURE:
 91 <221> NAME/KEY: MISC_FEATURE
 92 <222> LOCATION: (87)..(87)
 93 <223> OTHER INFORMATION: Xaa = an aromatic amino acid residue
 96 <220> FEATURE:
 97 <221> NAME/KEY: MISC_FEATURE
 98 <222> LOCATION: (89)..(89)
 99 <223> OTHER INFORMATION: Xaa = any amino acid residue
 102 <220> FEATURE:
 103 <221> NAME/KEY: MISC_FEATURE
 104 <222> LOCATION: (90)..(90)
 105 <223> OTHER INFORMATION: a hydrophobic amino acid residue
 108 <220> FEATURE:
 109 <221> NAME/KEY: MISC_FEATURE
 110 <222> LOCATION: (91)..(93)
 111 <223> OTHER INFORMATION: Xaa = any amino acid residue
 114 <400> SEQUENCE: 1
 W--> 116 Thr Leu Xaa Xaa Asp Pro Asp Glx Pro Xaa Xaa Xaa Asx Xaa Xaa
 117 1 5 10 15
 W--> 120 Xaa Xaa Glu Xaa Xaa His Xaa
 121 20 25 30
 W--> 124 Xaa
 125 35 40 45
 W--> 128 Xaa
 129 50 55 60
 W--> 132 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Tyr Xaa Xaa Xaa Xaa Pro Xaa Xaa
 133 65 70 75 80
 W--> 136 Xaa Xaa Gly Xaa His Arg Xaa Val Xaa Glx Xaa Xaa Xaa Gln
 137 85 90
 140 <210> SEQ ID NO: 2
 141 <211> LENGTH: 187
 142 <212> TYPE: PRT
 143 <213> ORGANISM: Homo sapiens
 145 <400> SEQUENCE: 2

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147 Met Pro Val Asp Leu Ser Lys Trp Ser Gly Pro Leu Ser Leu Gln Glu
 148 1 5 10 15
 151 Val Asp Glu Gln Pro Gln His Pro Leu His Val Thr Tyr Ala Gly Ala
 152 20 25 30
 155 Ala Val Asp Glu Leu Gly Lys Val Leu Thr Pro Thr Gln Val Lys Asn
 156 35 40 45
 159 Arg Pro Thr Ser Ile Ser Trp Asp Gly Leu Asp Ser Gly Lys Leu Tyr
 160 50 55 60
 163 Thr Leu Val Leu Thr Asp Pro Asp Ala Pro Ser Arg Lys Asp Pro Lys
 164 65 70 75 80
 167 Tyr Arg Glu Trp His His Phe Leu Val Val Asn Met Lys Gly Asn Asp
 168 85 90 95
 171 Ile Ser Ser Gly Thr Val Leu Ser Asp Tyr Val Gly Ser Gly Pro Pro
 172 100 105 110
 175 Lys Gly Thr Gly Leu His Arg Tyr Val Trp Leu Val Tyr Glu Gln Asp
 176 115 120 125
 179 Arg Pro Leu Lys Cys Asp Glu Pro Ile Leu Ser Asn Arg Ser Gly Lys
 180 130 135 140
 183 His Arg Gly Lys Phe Lys Val Ala Ser Phe Arg Lys Lys Tyr Glu Leu
 184 145 150 155 160
 187 Arg Ala Pro Val Ala Gly Thr Cys Tyr Gln Ala Glu Trp Lys Lys Tyr
 188 165 170 175
 191 Val Pro Lys Leu Tyr Glu Gln Leu Ser Gly Lys
 192 180 185
 195 <210> SEQ ID NO: 3
 196 <211> LENGTH: 187
 197 <212> TYPE: PRT
 198 <213> ORGANISM: Mus musculus
 200 <220> FEATURE:
 201 <221> NAME/KEY: MISC_FEATURE
 202 <222> LOCATION: (150)..(150)
 203 <223> OTHER INFORMATION: Xaa = any amino acid residue
 206 <400> SEQUENCE: 3
 208 Met Ala Ala Asp Ile Ser Gln Trp Ala Gly Pro Leu Cys Leu Gln Glu
 209 1 5 10 15
 212 Val Asp Glu Pro Pro Gln His Ala Leu Arg Val Asp Tyr Ala Gly Val
 213 20 25 30
 216 Thr Val Asp Glu Leu Gly Lys Val Leu Thr Pro Thr Gln Val Met Asn
 217 35 40 45
 220 Arg Pro Ser Ser Ile Ser Trp Asp Gly Leu Asp Pro Gly Lys Leu Tyr
 221 50 55 60
 224 Thr Leu Val Leu Thr Asp Pro Asp Ala Pro Ser Arg Lys Asp Pro Lys
 225 65 70 75 80
 228 Phe Arg Glu Trp His His Phe Leu Val Val Asn Met Lys Gly Asn Asp
 229 85 90 95
 232 Ile Ser Ser Gly Thr Val Leu Ser Asp Tyr Val Gly Ser Gly Pro Pro
 233 100 105 110
 236 Ser Gly Thr Ser Ile His Arg Tyr Val Trp Leu Val Tyr Glu Gln Glu
 237 115 120 125

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240 Gln Pro Leu Ser Cys Asp Glu Pro Ile Leu Ser Asn Lys Ser Gly Asp
 241 130 135 140
 WA-> 244 Asn Arg Gly Lys Phe Xaa Val Glu Thr Phe Arg Lys Lys Tyr Asn Leu
 245 145 150 155 160
 248 Gly Ala Pro Val Ala Gly Thr Cys Tyr Gln Ala Glu Trp Asp Asp Tyr
 249 165 170 175
 252 Val Pro Lys Leu Tyr Glu Gln Leu Ser Gly Lys
 253 180 185
 256 <210> SEQ ID NO: 4
 257 <211> LENGTH: 187
 258 <212> TYPE: PRT
 259 <213> ORGANISM: Drosophila
 261 <400> SEQUENCE: 4.
 263 Met Ser Asp Ser Thr Val Cys Phe Ser Lys His Lys Ile Val Pro Asp
 264 1 5 10 15
 267 Ile Leu Lys Thr Cys Pro Ala Thr Leu Leu Thr Val Thr Tyr Gly Gly
 268 20 25 30
 271 Gly Gln Val Val Asp Val Gly Gly Glu Leu Thr Pro Thr Gln Val Gln
 272 35 40 45
 275 Ser Gln Pro Lys Val Lys Trp Asp Ala Asp Pro Asn Ala Phe Tyr Thr
 276 50 55 60
 279 Leu Leu Leu Thr Asp Pro Asp Ala Pro Ser Arg Lys Glu Pro Lys Phe
 280 65 70 75 80
 283 Arg Glu Trp His His Trp Leu Val Val Asn Ile Pro Gly Asn Gln Val
 284 85 90 95
 287 Glu Asn Gly Val Val Leu Thr Glu Tyr Val Gly Ala Gly Pro Pro Gln
 288 100 105 110
 291 Gly Thr Gly Leu His Arg Tyr Val Phe Ile Val Phe Lys Gln Pro Gln
 292 115 120 125
 295 Lys Leu Thr Cys Asn Glu Pro Lys Ile Pro Lys Thr Ser Gly Asp Lys
 296 130 135 140
 299 Arg Ala Asn Phe Ser Thr Ser Lys Phe Met Ser Lys Tyr Lys Leu Gly
 300 145 150 155 160
 303 Asp Pro Ile Ala Gly Asn Phe Phe Gln Ala Gln Trp Asp Asp Tyr Val
 304 165 170 175
 307 Pro Lys Leu Tyr Lys Gln Leu Ser Gly Lys Lys
 308 180 185
 311 <210> SEQ ID NO: 5
 312 <211> LENGTH: 220
 313 <212> TYPE: PRT
 314 <213> ORGANISM: C. elegans
 316 <400> SEQUENCE: 5
 318 Met Val Val Leu Val Thr Arg Ser Leu Leu Pro Ala Leu Phe Phe Ala
 319 1 5 10 15
 322 Ser Arg Ala Pro Phe Ala Ala Ala Thr Thr Ser Ala Arg Phe Gln Arg
 323 20 25 30
 326 Gly Leu Ala Thr Met Ala Ala Glu Ala Phe Thr Lys His Glu Val Ile
 327 35 40 45
 330 Pro Asp Val Leu Ala Ser Asn Pro Pro Ser Lys Val Val Ser Val Lys

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331	50	55	60
334	Phe Asn Ser Gly Val Glu Ala Asn Leu Gly Asn Val Leu Thr Pro Thr		
335	65	70	75
338	Gln Val Lys Asp Thr Pro Glu Val Lys Trp Asp Ala Glu Pro Gly Ala		80
339	85	90	95
342	Leu Tyr Thr Leu Thr Lys Thr Asp Pro Asp Ala Pro Ser Arg Lys Glu		
343	100	105	110
346	Pro Thr Tyr Arg Glu Trp His His Trp Leu Val Val Asn Ile Pro Gly		
347	115	120	125
350	Asn Asp Ile Ala Lys Gly Asp Thr Leu Ser Glu Tyr Ile Gly Ala Gly		
351	130	135	140
354	Pro Pro Lys Thr Gly Leu His Arg Tyr Val Tyr Leu Ile Tyr Lys Gln		
355	145	150	155
358	Ser Gly Arg Ile Glu Asp Ala Glu His Gly Arg Leu Thr Asn Thr Ser		160
359	165	170	175
362	Gly Asp Lys Arg Gly Gly Trp Lys Ala Ala Asp Phe Val Ala Lys His		
363	180	185	190
366	Lys Leu Gly Ala Pro Val Phe Gly Asn Leu Phe Gln Ala Glu Tyr Asp		
367	195	200	205
370	Asp Tyr Val Pro Ile Leu Asn Lys Gln Leu Gly Ala		
371	210	215	220
374	<210> SEQ ID NO: 6		
375	<211> LENGTH: 181		
376	<212> TYPE: PRT		
377	<213> ORGANISM: Antirrhinum-CEN		
379	<400> SEQUENCE: 6		
381	Met Ala Ala Lys Val Ser Ser Asp Pro Leu Val Ile Gly Arg Val Ile		
382	1	5	10
385	Gly Asp Val Val Asp His Phe Thr Ser Thr Val Lys Met Ser Val Ile		15
386	20	25	30
389	Tyr Asn Ser Asn Asn Ser Ile Lys His Val Tyr Asn Gly His Glu Leu		
390	35	40	45
393	Phe Pro Ser Ala Val Thr Ser Thr Pro Arg Val Glu Val His Gly Gly		
394	50	55	60
397	Asp Met Arg Ser Phe Phe Thr Leu Ile Met Thr Asp Pro Asp Val Pro		
398	65	70	75
401	Gly Pro Ser Asp Pro Tyr Leu Arg Glu His Leu His Trp Ile Val Thr		80
402	85	90	95
405	Asp Ile Pro Gly Thr Thr Asp Ser Ser Phe Gly Lys Glu Val Val Ser		
406	100	105	110
409	Tyr Glu Met Pro Arg Pro Asn Ile Gly Ile His Arg Phe Val Phe Leu		
410	115	120	125
413	Leu Phe Lys Gln Lys Lys Arg Gly Gln Ala Met Leu Ser Pro Pro Val		
414	130	135	140
417	Val Cys Arg Asp Gly Phe Asn Thr Arg Lys Phe Thr Gln Glu Asn Glu		
418	145	150	155
421	Leu Gly Leu Pro Val Ala Ala Val Phe Phe Asn Cys Gln Arg Glu Thr		160
422	165	170	175
425	Ala Ala Arg Arg Arg		

→ Use of n and/or Xaa has been detected in the Sequence Listing.
 Review the Sequence Listing to insure a corresponding
 explanation is presented in the <220> to <223> fields of
 each sequence using n or Xaa.

VERIFICATION SUMMARY DATE: 02/06/2002
PATENT APPLICATION: US/09/654,281B TIME: 08:50:54

Input Set : A:\ES.txt
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L:116 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:120 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:124 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:128 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:132 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:136 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:244 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:561 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:10
L:575 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:581 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:11